RAW SEQUENCE LISTING

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Application Serial Number: 10/552,298
Source: PCT
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RAW SEQUENCE LISTING DATE: 10/18/2005
PATENT APPLICATION: **US/10/552,298** TIME: 10:10:33

Input Set : **A:\034123-168 - Sequence Listing.txt**
Output Set: **N:\CRF4\10182005\J552298.raw**

<110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
GILL, Gordon N.
YEO, Michele
LIN, Patrick S.
DAHMUS, Michael E.
<120> TITLE OF INVENTION: PHOSPHATASE REGULATION OF NUCLEIC ACID TRANSCRIPTION
<130> FILE REFERENCE: UCSD1870WO
C--> **<140> CURRENT APPLICATION NUMBER: US/10/552,298**
C--> **<141> CURRENT FILING DATE: 2005-09-30**
<150> PRIOR APPLICATION NUMBER: US 60/459,786
<151> PRIOR FILING DATE: 2003-04-01
<160> NUMBER OF SEQ ID NOS: 67
<170> SOFTWARE: PatentIn version 3.3
<210> SEQ ID NO: 1
<211> LENGTH: 783
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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ggcaaaggtg accagaagtc agcagcttcc cagaagcccc gaagccgggg catcctccac    120
tcactcttct gctgtgtctg ccgggatgat ggggaggccc tgcctgctca cagcggggcg    180
cccctgcttg tggaggagaa tggcgccatc cctaagaccc cagtccaata cctgctccct    240
gaggccaagg cccaggactc agacaagatc tgcgtggtca tcgacctgga cgagaccctg    300
gtgcacagct ccttcaagcc agtgaacaac gcggacttca tcatccctgt ggagattgat    360
ggggtggtcc accaggtcta cgtgttgaag cgtcctcatg tggatgagtt cctgcagcga    420
atgggcgagc tctttgaatg tgtgctgttc actgctagcc tcgccaagta cgcagaccca    480
gtagctgacc tgctggacaa atgggggcc ttccgggccc ggctgtttcg agagtcctgc    540
gtcttccacc gggggaacta cgtgaaggac ctgagccggt tgggtcgaga cctgcggcgg    600
gtgctcatcc tggacaattc acctgcctcc tatgtcttcc atccagacaa tgctgtaccg    660
gtggcctcgt ggtttgacaa catgagtgac acagagctcc acgacctcct ccccttcttc    720
gagcaactca gccgtgtgga cgacgtgtac tcagtgctca ggcagccacg gccagggagc    780
tag                                                                  783
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<210> SEQ ID NO: 2
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

```
Met Asp Ser Ser Ala Val Ile Thr Gln Ile Ser Lys Glu Glu Ala Arg
1               5                  10                  15
Gly Pro Leu Arg Gly Lys Gly Asp Gln Lys Ser Ala Ala Ser Gln Lys
            20                  25                  30
Pro Arg Ser Arg Gly Ile Leu His Ser Leu Phe Cys Cys Val Cys Arg
        35                  40                  45
```

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```
77 Asp Asp Gly Glu Ala Leu Pro Ala His Ser Gly Ala Pro Leu Leu Val
78     50                  55                  60
81 Glu Glu Asn Gly Ala Ile Pro Lys Thr Pro Val Gln Tyr Leu Leu Pro
82 65                  70                  75                  80
85 Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp Leu
86                 85                  90                  95
89 Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala Asp
90             100                 105                 110
93 Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr Val
94         115                 120                 125
97 Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu Leu
98     130                 135                 140
101 Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro
102 145                 150                 155                 160
105 Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu Phe
106                 165                 170                 175
109 Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu Ser
110             180                 185                 190
113 Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser Pro
114         195                 200                 205
117 Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser Trp
118     210                 215                 220
121 Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe Phe
122 225                 230                 235                 240
125 Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln Pro
126                 245                 250                 255
129 Arg Pro Gly Ser
130             260
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 852
135 <212> TYPE: DNA
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
139 atggaacacg gctccatcat cacccaggcg cggagggaag acgccctggt gctcaccaag     60
141 caaggcctgg tctccaagtc ctctcctaag aagcctcgtg gacgtaacat cttcaaggcc    120
143 cttttctgct gttttcgcgc ccagcatgtt ggccagtcaa gttcctccac tgagctcgct    180
145 gcgtataagg aggaagcaaa caccattgct aagtcggatc tgctccagtg tctccagtac    240
147 cagttctacc agatcccagg gacctgcctg ctcccagagg tgacagagga agatcaagga    300
149 aggatctgtg tggtcattga cctcgatgaa acccttgtgc atagctcctt taagccaatc    360
151 aacaatgctg acttcatagt gcctatagag attgagggga ccactcacca ggtgtatgtg    420
153 ctcaagaggc cttatgtgga tgagttcctg agacgcatgg gggaactctt tgaatgtgtt    480
155 ctcttcactg ccagcctggc caagtatgcc gaccctgtga cagacctgct ggaccggtgt    540
157 ggggtgttcc gggcccgcct attccgtgag tcttgcgtgt tccaccaggg ctgctacgtc    600
159 aaggacctca gccgcctggg gagggacctg agaaagaccc tcatcctgga caactcgcct    660
161 gcttcttaca tattccaccc cgagaatgca gtgcctgtgc agtcctggtt tgatgacatg    720
163 gcagacactg agttgctgaa cctgatccca atctttgagg agctgagcgg agcagaggac    780
165 gtctacacca gccttggggc agctgcgggc cccttagcct gccctgcttc caagcgacgg    840
167 ccatcccagt ag                                                      852
170 <210> SEQ ID NO: 4
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<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 4

Met	Glu	His	Gly	Ser	Ile	Ile	Thr	Gln	Ala	Arg	Arg	Glu	Asp	Ala	Leu
1				5				10						15	
Val	Leu	Thr	Lys	Gln	Gly	Leu	Val	Ser	Lys	Ser	Ser	Pro	Lys	Lys	Pro
			20					25					30		
Arg	Gly	Arg	Asn	Ile	Phe	Lys	Ala	Leu	Phe	Cys	Cys	Phe	Arg	Ala	Gln
		35					40					45			
His	Val	Gly	Gln	Ser	Ser	Ser	Ser	Thr	Glu	Leu	Ala	Ala	Tyr	Lys	Glu
	50					55					60				
Glu	Ala	Asn	Thr	Ile	Ala	Lys	Ser	Asp	Leu	Leu	Gln	Cys	Leu	Gln	Tyr
65					70					75					80
Gln	Phe	Tyr	Gln	Ile	Pro	Gly	Thr	Cys	Leu	Leu	Pro	Glu	Val	Thr	Glu
				85					90					95	
Glu	Asp	Gln	Gly	Arg	Ile	Cys	Val	Val	Ile	Asp	Leu	Asp	Glu	Thr	Leu
			100					105					110		
Val	His	Ser	Ser	Phe	Lys	Pro	Ile	Asn	Asn	Ala	Asp	Phe	Ile	Val	Pro
		115					120					125			
Ile	Glu	Ile	Glu	Gly	Thr	Thr	His	Gln	Val	Tyr	Val	Leu	Lys	Arg	Pro
	130					135					140				
Tyr	Val	Asp	Glu	Phe	Leu	Arg	Arg	Met	Gly	Glu	Leu	Phe	Glu	Cys	Val
145					150					155					160
Leu	Phe	Thr	Ala	Ser	Leu	Ala	Lys	Tyr	Ala	Asp	Pro	Val	Thr	Asp	Leu
				165					170					175	
Leu	Asp	Arg	Cys	Gly	Val	Phe	Arg	Ala	Arg	Leu	Phe	Arg	Glu	Ser	Cys
			180					185					190		
Val	Phe	His	Gln	Gly	Cys	Tyr	Val	Lys	Asp	Leu	Ser	Arg	Leu	Gly	Arg
		195					200					205			
Asp	Leu	Arg	Lys	Thr	Leu	Ile	Leu	Asp	Asn	Ser	Pro	Ala	Ser	Tyr	Ile
	210					215					220				
Phe	His	Pro	Glu	Asn	Ala	Val	Pro	Val	Gln	Ser	Trp	Phe	Asp	Asp	Met
225					230					235					240
Ala	Asp	Thr	Glu	Leu	Leu	Asn	Leu	Ile	Pro	Ile	Phe	Glu	Glu	Leu	Ser
				245					250					255	
Gly	Ala	Glu	Asp	Val	Tyr	Thr	Ser	Leu	Gly	Ala	Ala	Ala	Gly	Pro	Leu
			260					265					270		
Ala	Cys	Pro	Ala	Ser	Lys	Arg	Arg	Pro	Ser	Gln					
		275					280								

<210> SEQ ID NO: 5
<211> LENGTH: 798
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 5

atggacggcc cggccatcat cacccaggtg accaacccca aggaggacga gggccggttg 60
ccgggcgcgg gcgagaaagc ctcccagtgc aacgtcagct taaagaagca gaggagccgc 120
agcatcctta gctccttctt ctgctgcttc cgtgattaca atgtggaggc ccctccaccc 180
agcagcccca gtgtgcttcc gccactggtg gaggagaatg gtgggcttca gaagccacca 240

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gctaagtacc ttcttccaga ggtgacggtg cttgactatg gaaagaaatg tgtggtcatt 300
gatttagatg aaacattggt gcacagttcg tttaagccta ttagtaatgc tgattttatt 360
gttccggttg aaatcgatgg aactatacat caggtgtatg tgctgaagcg gccacatgtg 420
gacgagttcc tccagaggat ggggcagctt tttgaatgtg tgctctttac tgccagcttg 480
gccaagtatg cagaccctgt ggctgacctc ctagaccgct ggggtgtgtt ccgggcccgg 540
ctcttcagag aatcatgtgt ttttcatcgt gggaactacg tgaaggacct gagtcgcctt 600
gggcgggagc tgagcaaagt gatcattgtt gacaattccc ctgcctcata catcttccat 660
cctgagaatg cagtgcctgt gcagtcctgg ttcgatgaca tgacggacac ggagctgctg 720
gacctcatcc ccttctttga gggcctgagc cgggaggacg acgtgtacag catgctgcac 780
agactctgca ataggtag 798

<210> SEQ ID NO: 6
<211> LENGTH: 265
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 6

Met Asp Gly Pro Ala Ile Ile Thr Gln Val Thr Asn Pro Lys Glu Asp
1 5 10 15
Glu Gly Arg Leu Pro Gly Ala Gly Glu Lys Ala Ser Gln Cys Asn Val
20 25 30
Ser Leu Lys Lys Gln Arg Ser Arg Ser Ile Leu Ser Ser Phe Phe Cys
35 40 45
Cys Phe Arg Asp Tyr Asn Val Glu Ala Pro Pro Pro Ser Ser Pro Ser
50 55 60
Val Leu Pro Pro Leu Val Glu Glu Asn Gly Gly Leu Gln Lys Pro Pro
65 70 75 80
Ala Lys Tyr Leu Leu Pro Glu Val Thr Val Leu Asp Tyr Gly Lys Lys
85 90 95
Cys Val Val Ile Asp Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys
100 105 110
Pro Ile Ser Asn Ala Asp Phe Ile Val Pro Val Glu Ile Asp Gly Thr
115 120 125
Ile His Gln Val Tyr Val Leu Lys Arg Pro His Val Asp Glu Phe Leu
130 135 140
Gln Arg Met Gly Gln Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu
145 150 155 160
Ala Lys Tyr Ala Asp Pro Val Ala Asp Leu Leu Asp Arg Trp Gly Val
165 170 175
Phe Arg Ala Arg Leu Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn
180 185 190
Tyr Val Lys Asp Leu Ser Arg Leu Gly Arg Glu Leu Ser Lys Val Ile
195 200 205
Ile Val Asp Asn Ser Pro Ala Ser Tyr Ile Phe His Pro Glu Asn Ala
210 215 220
Val Pro Val Gln Ser Trp Phe Asp Asp Met Thr Asp Thr Glu Leu Leu
225 230 235 240
Asp Leu Ile Pro Phe Phe Glu Gly Leu Ser Arg Glu Asp Asp Val Tyr
245 250 255
Ser Met Leu His Arg Leu Cys Asn Arg
260 265

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Input Set : A:\034123-168 - Sequence Listing.txt
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<210> SEQ ID NO: 7
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 7
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ccatccctaa ggcagacccc agtccaatac ctgctccctg aggccaaggc ccaggactca 120
gacaagatct gcgtggtcat cgacctggac gagaccctgg tgcacagctc cttcaagcca 180
gtgaacaacg cggacttcat catccctgtg gagattgatg gggtggtcca ccaggtctac 240
gtgttgaagc gtcctcacgt ggatgagttc ctgcagcgaa tgggcgagct ctttgaatgt 300
gtgctgttca ctgctagcct cgccaagtac gcagacccag tagctgacct gctggacaaa 360
tgggggcct tccgggcccg gctgtttcga gagtcctgcg tcttccaccg ggggaactac 420
gtgaaggacc tgagccggtt gggtcgagac ctgcggcggg tgctcatcct ggacaattca 480
cctgcctcct atgtcttcca tccagacaat gctgtaccgg tggcctcgtg gtttgacaac 540
atgagtgaca cagagctcca cgacctcctc cccttcttcg agcaactcag ccgtgtggac 600
gacgtgtact cagtgctcag gcagccacgg ccagggagct ag 642
<210> SEQ ID NO: 8
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 8
Met Met Gly Arg Pro Cys Leu Leu Thr Ala Gly Arg Pro Cys Leu Trp
1 5 10 15
Arg Arg Met Ala Pro Ser Leu Arg Gln Thr Pro Val Gln Tyr Leu Leu
20 25 30
Pro Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp
35 40 45
Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala
50 55 60
Asp Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr
65 70 75 80
Val Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu
85 90 95
Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp
100 105 110
Pro Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu
115 120 125
Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu
130 135 140
Ser Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser
145 150 155 160
Pro Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser
165 170 175
Trp Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe
180 185 190
Phe Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln
195 200 205
Pro Arg Pro Gly Ser
210

VERIFICATION SUMMARY DATE: 10/18/2005
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Input Set : **A:\034123-168 - Sequence Listing.txt**
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date